

AMENDMENTS TO THE SPECIFICATION

At page 1, please amend the title as follows.

~~Novel neurotrophic~~ Neurotrophic factor protein and uses thereof

Please replace the paragraph on page 6 at line 9 as follows:

Figure 3. Alignment of MANF amino acid sequences from selected organisms. The sequences were acquired by running Blast searches at the National Center for Biotechnology information's www-server (www.ncbi.nlm.nih.gov). (~~http://www.ncbi.nlm.nih.gov~~). In some cases the sequence was assembled from the genomic sequence and in some cases by assembling overlapping expressed sequence tags.

Please replace the paragraph on page 20 at line 6 as follows:

To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997, Nucleic Acids Res. 25: 3389-3402). Alternatively, PSI-Blast or PHI-Blast can be used to perform an iterated search which detects distant relationships between molecules and relationships between molecules which share a common pattern. When utilizing BLAST, Gapped BLAST, PSI-Blast and PHI-Blast programs, the default parameters of the respective programs (e.g. XBLAST and NBLAST) can be used. See ~~http~~ [://www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov) www.ncbi.nlm.nih.gov.

Please replace Table A on page 11 with the following amended Table A.

Table A

MANF1 vs MANF2

Amino acid identity (%)*

	Hs-MANF1 <u>Hs-MANF1</u>	Hs-MANF2	Mm-MANF1	Mm-MANF2
Hs-MANF1	100	-	-	-
Hs-MANF2	65	100	-	-
Mm-MANF1	98	63	100	-
Mm-MANF2	65	80	65	100

Amino acid similarity (%)*

	Hs-MANF1 <u>Hs-MANF1</u>	Hs-MANF2	Mm-MANF1	Mm-MANF2
Hs-MANF1	100	-	-	-
Hs-MANF2	79	100	-	-
Mm-MANF1	98	78	100	-
Mm-MANF2	78	88	78	100

* Signal sequences omitted

Please replace the paragraph on page at line 15 as follows:

To study if MANF2 protein is secreted we generated expression constructs encoding V5-His-tagged human MANF2 fusion proteins and analyzed their expression and secretion in ~~Cos-7 cells~~ Cos-7 cells. The results show that MANF2 is a secreted ~20 kDa protein, with potential glycosylation and/or posttranslational processing (cleavage) involved (Fig. 6).